

Genetic Analysis of a Vancomycin-Resistant *Staphylococcus aureus* Strain Isolated in Iran

In their recent paper, Kobayashi et al. evaluated the emergence of vancomycin-resistant *Staphylococcus aureus* (VRSA) by genomic analysis (1). Based on whole-genome sequencing data for all U.S. VRSA strains isolated to date (2), they proposed that the development of resistance to vancomycin is an independent event in VRSA strains. It was our pleasure to read their article. We found that our results are in concordance with their conclusions. Our VRSA isolate belongs to ST1283, CC8, *Spa* t037, *SCCmec* III, and *agrI* (3). These genetic features are specific to endemic Asian clones and distinct from those of U.S. VRSA isolates, which all belonged to CC5. Moreover, the plasmids of our VRSA isolate were different from routine VRSA plasmids, based on the HindIII digestion pattern and multiplex PCR for common staphylococcal or enterococcal plasmids (our unpublished data). Collectively, these data indicate that our VRSA isolate is different from previously described isolates and probably carries an uncommon type of *vanA*-containing plasmid. These findings support the assumption made by Kobayashi et al. regarding independent acquisition of *vanA* by *S. aureus* in different geographical areas. Hopefully, our future whole-genome sequencing of this strain will shed light on the matter.

To conclude, it seems that the spread of vancomycin-resistant *S. aureus* across the globe is not due to the circulation of a specific resistant strain, and therefore, this could constitute an advance warning about the dissemination of VRSA strains with local origins of resistance.

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